

ADM72285

ID ADM72285 standard; protein; 1030 AA.

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AC ADM72285;

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DT 17-JUN-2004 (first entry)

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DE Porcine TLR9 polypeptide.

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KW TLR9; toll-like receptor 9; CpG; TLR9 signaling; porcine.

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OS Sus scrofa.

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PN WO2004026888-A2.

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PD 01-APR-2004.

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PF 19-SEP-2003; 2003WO-US029577.

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PR 19-SEP-2002; 2002US-0412479P.

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PA (COLE-) COLEY PHARM GMBH.

PA (UYSA-) UNIV SASKATCHEWAN.

PA (QIAG-) QIAGEN GMBH.

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PI Lipford GB, Mookherjee N, Babiuk L, Brownlie R, Griebel P;

PI Mutwiri G, Hecker R;

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DR WPI; 2004-295374/27.

DR N-PSDB; ADM72287.

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PT New polypeptide, useful for identifying key amino acids in a TLR9 of a
 PT first species which confer specificity for CpG DNA optimized for TLR9 of
 PT the first species.

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PS Claim 1; SEQ ID NO 5; 170pp; English.

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CC The invention relates to novel Toll-like receptor 9 (TLR9) polypeptides
 CC and encoding polynucleotides. It provides methods for (i) identifying key
 CC amino acids in a TLR9 of a first species which confer specificity for CpG
 CC DNA optimized for TLR9 of the first species; (ii) identifying key amino
 CC acids in human TLR9 which confer specificity for CpG DNA optimized for
 CC human TLR9; (iii) identify a TLR9 ligand; and (iv) identify species-
 CC specific CpG-motif preference of the isolated polypeptide. The screening
 CC method to identify species-specific CpG-motif preference of the isolated
 CC polypeptide comprises: contacting an isolated polypeptide with a CpG DNA
 CC comprising a hexamer sequence consisting of GACGTT, AACGTT, CACGTT,
 CC TACGTT, GCGGTT, GCCGTT, GTCGTT, GATGTT, GAAGTT, GAGGTT, GACATT, GACCTT,
 CC GACTTT, GACGCT, GACGAT, GACGGT, GACGTC, GACGTA and GACGTG; measuring a
 CC signal in response to the contacting; and identifying a species-specific
 CC CpG-motif preference when the signal in response to the contacting is
 CC consistent with TLR9 signaling. The signal comprises expression of a
 CC reporter gene responsive to TLR/IL-1R signal transduction pathway. The
 CC reporter gene is operatively linked to a promoter sensitive to NF-KB. The
 CC CpG DNA is an oligodeoxynucleotide having a sequence consisting of
 CC sequences selected from ADM72319- ADM72337. The polypeptide is useful for
 CC identifying key amino acids in a TLR9 of a first species which confer
 CC specificity for CpG DNA optimized for TLR9 of the first species. The
 CC present sequence represents a porcine TLR9 polypeptide

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SQ Sequence 1030 AA;

Alignment Scores:

Length:	1030		
Score:	5400.00	Matches:	1026
Percent Similarity:	99.6%	Conservative:	0
Best Local Similarity:	99.6%	Mismatches:	4
Query Match:	86.4%	Indels:	0
DB:	1	Gaps:	0

US-10-561-022-1 (1-3329) x ADM72285 (1-1030)

Qy	55	ATGGGCCCCCGCTGCACCCTGCACCCCTTTCTCTCCTGGTGCAGGTGACAGCGCTGGCT	114
Db	1	MetGlyProArgCysThrLeuHisProLeuSerLeuLeuValGlnValThrAlaLeuAla	20
Qy	115	GCGACTCTGGCCCAGGGCAGGCTGCCTGCCTTCTGCCCTGTGAGCTCCAGCCCCACGGC	174
Db	21	AlaAlaLeuAlaGlnGlyArgLeuProAlaPheLeuProCysGluLeuGlnProHisGly	40
Qy	175	CTGGTGAAGTCAACTGGCTCTTCTGAAGTCCGTGCCCCACTTCTCGGCGGCAGCGCCC	234
Db	41	LeuValAsnCysAsnTrpLeuPheLeuLysSerValProHisPheSerAlaAlaAlaPro	60
Qy	235	CGGGCCAACGTCACCAGCCTCTCCTTACTCTCCAACCGCATCCACCACTTGCACGACTCT	294
Db	61	ArgAlaAsnValThrSerLeuSerLeuLeuSerAsnArgIleHisHisLeuHisAspSer	80
Qy	295	GACTTCGTCCACCTGTCCAGCCTACGAACCTCTCAACCTCAAGTGGAAGTGGCCGCCGGCT	354
Db	81	AspPheValHisLeuSerSerLeuArgThrLeuAsnLeuLysTrpAsnCysProProAla	100
Qy	355	GGCCTCAGCCCCATGCACCTCCCCTGCCACATGACCATCGAGCCCAACACCTTCTGGCC	414
Db	101	GlyLeuSerProMetHisPheProCysHisMetThrIleGluProAsnThrPheLeuAla	120
Qy	415	GTGCCCACCCTGGAGGAGCTGAACCTGAGCTACAACAGCATCACGACCGTGCCTGCCCTG	474
Db	121	ValProThrLeuGluGluLeuAsnLeuSerTyrAsnSerIleThrThrValProAlaLeu	140
Qy	475	CCCGACTCCCTCGTGTCCCTGTGCTGAGCCGCACCAACATCCTGGTGCTAGACCCACC	534
Db	141	ProAspSerLeuValSerLeuSerLeuSerArgThrAsnIleLeuValLeuAspProThr	160
Qy	535	CACCTCACTGGCCTACATGCCCTGCGCTACCTGTACATGGATGGCAACTGCTACTACAAG	594
Db	161	HisLeuThrGlyLeuHisAlaLeuArgTyrLeuTyrMetAspGlyAsnCysTyrTyrLys	180
Qy	595	AACCCCTGCCAGGGGGCGCTGGAGGTGGTGCCGGGTGCCCTCCTCGGCCTGGGCAACCTC	654
Db	181	AsnProCysGlnGlyAlaLeuGluValValProGlyAlaLeuLeuGlyLeuGlyAsnLeu	200
Qy	655	ACACATCTCTCACTCAAGTACAACAATCTCACGGAGGTGCCCCGAGCCTGCCCCCAGC	714
Db	201	ThrHisLeuSerLeuLysTyrAsnAsnLeuThrGluValProArgSerLeuProProSer	220
Qy	715	CTGGAGACCCTGCTGTTGTCTACAACCACATTGTCACCCTGACGCCTGAGGACCTGGCC	774
Db	221	LeuGluThrLeuLeuLeuSerTyrAsnHisIleValThrLeuThrProGluAspLeuAla	240
Qy	775	AATCTGACTGCCCTGCGCGTGCTTGATGTGGGGGGAAGTGCCGCCGCTGTGACCATGCC	834

Db	241	AsnLeuThrAlaLeuArgValLeuAspValGlyGlyAsnCysArgArgCysAspHisAla	260
Qy	835	CGCAACCCCTGCAGGGAGTGCCCAAAGGACCACCCCAAGCTGCACTCTGACACCTTCAGC	894
Db	261	ArgAsnProCysArgGluCysProLysAspHisProLysLeuHisSerAspThrPheSer	280
Qy	895	CACCTGAGCCGCTCGAAGGCCTGGTGTGAAAGACAGTTCTCTCTACAACCTGGACGCC	954
Db	281	HisLeuSerArgLeuGluGlyLeuValLeuLysAspSerSerLeuTyrAsnLeuAspThr	300
Qy	955	AGGTGGTTCCGAGGCCTGGACAGGCTCCAAGTGCTGGACCTGAGTGAGAACTTCCTCTAC	1014
Db	301	ArgTrpPheArgGlyLeuAspArgLeuGlnValLeuAspLeuSerGluAsnPheLeuTyr	320
Qy	1015	GACTGCATCACCAAGACCACGGCCTTCCAGGGCCTGGCCCGACTGCGCAAGCTCAACCTG	1074
Db	321	AspCysIleThrLysThrThrAlaPheGlnGlyLeuAlaArgLeuArgSerLeuAsnLeu	340
Qy	1075	TCCTTCAATTACCACAAGAAGGTGTCCTTTGCCACCTGCACCTGGCACCTTCCTTTGGG	1134
Db	341	SerPheAsnTyrHisLysLysValSerPheAlaHisLeuHisLeuAlaProSerPheGly	360
Qy	1135	CACCTCCGGTCCCTGAAGGAGCTGGACATGCATGGCATCTTCTTCCGCTCGCTCAGTGAG	1194
Db	361	HisLeuArgSerLeuLysGluLeuAspMetHisGlyIlePhePheArgSerLeuSerGlu	380
Qy	1195	ACCACGCTCCAACCTCTGGTCCAACCTGCCTATGCTCCAGACCCTGCGCCTGCAGATGAAC	1254
Db	381	ThrThrLeuGlnProLeuValGlnLeuProMetLeuGlnThrLeuArgLeuGlnMetAsn	400
Qy	1255	TTCATTAACCAGGCCAGCTCAGCATCTTTGGGGCCTTCCCTGGCCTGCTGTACGTGGAC	1314
Db	401	PheIleAsnGlnAlaGlnLeuSerIlePheGlyAlaPheProGlyLeuLeuTyrValAsp	420
Qy	1315	CTATCGGACAACCGCATCAGCGGAGCTGCAAGGCCAGTGGCCATTACTAGGGAGGTGGAT	1374
Db	421	LeuSerAspAsnArgIleSerGlyAlaAlaArgProValAlaIleThrArgGluValAsp	440
Qy	1375	GGTAGGGAGAGGTCTGGCTGCCTTCCAGGAACCTCGCTCCACGTCCACTGGACACTCTC	1434
Db	441	GlyArgGluArgValTrpLeuProSerArgAsnLeuAlaProArgProLeuAspThrLeu	460
Qy	1435	CGCTCAGAGGACTTCATGCCAACTGCAAGGCCTTCAGCTTCACCTTGACCTGTCTCGG	1494
Db	461	ArgSerGluAspPheMetProAsnCysLysAlaPheSerPheThrLeuAspLeuSerArg	480
Qy	1495	AACAACCTGGTGACAATCCAGTCGGAGATGTTTGCTCGCCTCTCACGCCTCGAGTGCCTG	1554
Db	481	AsnAsnLeuValThrIleGlnSerGluMetPheAlaArgLeuSerArgLeuGluCysLeu	500
Qy	1555	CGTCTGAGCCACAACAGCATCTCCCAGGCGGTCAATGGCTCTCAGTTTGTGCCGCTGACC	1614
Db	501	ArgLeuSerHisAsnSerIleSerGlnAlaValAsnGlySerGlnPheValProLeuThr	520
Qy	1615	AGCCTGCGGGTGCTGGACCTGTCCCACAACAAGCTGGACCTGTATCACGGGCGCTCGTTC	1674
Db	521	SerLeuArgValLeuAspLeuSerHisAsnLysLeuAspLeuTyrHisGlyArgSerPhe	540
Qy	1675	ACGGAGCTGCCGCGCCTGGAAGCACTGGACCTCAGCTACAACAGCCAGCCCTTTACCATG	1734
Db	541	ThrGluLeuProArgLeuGluAlaLeuAspLeuSerTyrAsnSerGlnProPheThrMet	560

Qy	1735	CAGGGTGTGGGCCACAACCTCAGCTTCGTGGCCAGCTGCCCCGCCCTGCGCTACCTCAGC	1794
Db	561	GlnGlyValGlyHisAsnLeuSerPheValAlaGlnLeuProAlaLeuArgTyrLeuSer	580
Qy	1795	CTGGCGCACAAATGACATCCATAGCCGAGTGTCAGCAGCTCTGTAGCGCCTCACTGTGC	1854
Db	581	LeuAlaHisAsnAspIleHisSerArgValSerGlnGlnLeuCysSerAlaSerLeuCys	600
Qy	1855	GCCCTGGACTTTAGCGGCAACGATCTGAGCCGGATGTGGGCTGAGGGAGACCTCTATCTC	1914
Db	601	AlaLeuAspPheSerGlyAsnAspLeuSerArgMetTrpAlaGluGlyAspLeuTyrLeu	620
Qy	1915	CGCTTCTTCCAAGGCCTAAGAAGCCTAGTCTGGCTGGACCTGTCCCAGAACCACCTGCAC	1974
Db	621	ArgPhePheGlnGlyLeuArgSerLeuValTrpLeuAspLeuSerGlnAsnHisLeuHis	640
Qy	1975	ACCCTCCTGCCACGTGCCCTGGACAACCTCCCCAAAAGCCTGAAGCATCTGCATCTCCGT	2034
Db	641	ThrLeuLeuProArgAlaLeuAspAsnLeuProLysSerLeuLysHisLeuHisLeuArg	660
Qy	2035	GACAATAACCTGGCCTTCTTCAACTGGAGCAGCCTGACCCTCCTGCCCCAAGCTGGAAACC	2094
Db	661	AspAsnAsnLeuAlaPhePheAsnTrpSerSerLeuThrLeuLeuProLysLeuGluThr	680
Qy	2095	CTGGACTTGGCTGGAAACCAGCTGAAGGCCCTAAGCAATGGCAGCCTGCCATCTGGCACC	2154
Db	681	LeuAspLeuAlaGlyAsnGlnLeuLysAlaLeuSerAsnGlySerLeuProSerGlyThr	700
Qy	2155	CAGCTGCGGAGGCTGGACCTCAGTGGCAACAGCATCGGCTTTGTGAACCCTGGCTTCTTT	2214
Db	701	GlnLeuArgArgLeuAspLeuSerGlyAsnSerIleGlyPheValAsnProGlyPhePhe	720
Qy	2215	GCCCTGGCCAAGCAGTTAGAAGAGCTCAACCTCAGCGCCAATGCCCTCAAGACAGTGGAG	2274
Db	721	AlaLeuAlaLysGlnLeuGluGluLeuAsnLeuSerAlaAsnAlaLeuLysThrValGlu	740
Qy	2275	CCCTCCTGGTTTGGCTCGATGGTGGGCAACCTGAAAGTCCTAGACGTGAGCGCCAACCCT	2334
Db	741	ProSerTrpPheGlySerMetValGlyAsnLeuLysValLeuAspValSerAlaAsnPro	760
Qy	2335	CTGCACTGCGCCTGTGGGGCGACCTTCGTGGGCTTCCTGCTGGAGGTACAGGCTGCCGTG	2394
Db	761	LeuHisCysAlaCysGlyAlaThrPheValGlyPheLeuLeuGluValGlnAlaAlaVal	780
Qy	2395	CCTGGGCTGCCCAGCCGCGTCAAGTGTGGCAGTCCGGGGCAGCTCCAGGGCCATAGCATC	2454
Db	781	ProGlyLeuProSerArgValLysCysGlySerProGlyGlnLeuGlnGlyHisSerIle	800
Qy	2455	TTTGCGCAAGACCTGCGCCTCTGCCTGGATGAGACCCTCTCGTGGAAGTGTGTTTGGCATC	2514
Db	801	PheAlaGlnAspLeuArgLeuCysLeuAspGluThrLeuSerTrpAsnCysPheGlyIle	820
Qy	2515	TCGCTGCTGGCCATGGCCCTGGGCTGGTTGTGCCCATGCTGCACCACCTCTGCGGCTGG	2574
Db	821	SerLeuLeuAlaMetAlaLeuGlyLeuValValProMetLeuHisHisLeuCysGlyTrp	840
Qy	2575	GACCTCTGGTACTGCTTCCACCTGTGCCTGGCCTGGCTGCCCCACCGAGGGCAGCGCGG	2634
Db	841	AspLeuTrpTyrCysPheHisLeuCysLeuAlaTrpLeuProHisArgGlyGlnArgArg	860

Qy	2635	GGCGCAGACGCCCTGTTCTATGATGCCTTCGTGGTCTTTGACAAAGCTCAGAGTGCTGTG	2694
Db	861	GlyAlaAspAlaLeuPheTyrAspAlaPheValValPheAspLysAlaGlnSerAlaVal	880
Qy	2695	GCCGACTGGGTGTACAACGAGCTGCGGGTGCAGCTGGAGGAGCGCCGTGGGCGCCGCGCA	2754
Db	881	AlaAspTrpValTyrAsnGluLeuArgValGlnLeuGluGluArgArgGlyArgArgAla	900
Qy	2755	CTGCGCCTGTGCCTGGAGGAGCGAGACTGGTTACCTGGCAAGACGCTCTTCGAGAACCTG	2814
Db	901	LeuArgLeuCysLeuGluGluArgAspTrpLeuProGlyLysThrLeuPheGluAsnLeu	920
Qy	2815	TGGGCCTCAGTCTACAGCAGCCGCAAGACCCTGTTTGTGCTGGCCCACACGGACCGTGTC	2874
Db	921	TrpAlaSerValTyrSerSerArgLysThrLeuPheValLeuAlaHisThrAspArgVal	940
Qy	2875	AGCGGCCTCTTGCGTGCCAGTTTCCTGCTGGCCCAGCAGCGCCTGCTGGAGGACCGCAAG	2934
Db	941	SerGlyLeuLeuArgAlaSerPheLeuLeuAlaGlnGlnArgLeuLeuGluAspArgLys	960
Qy	2935	GACGTTGTAGTGCTGGTGATCCTGCGCCCCGATGCCTACCGCTCCCGCTACGTGCGGCTG	2994
Db	961	AspValValValLeuValIleLeuArgProAspAlaTyrArgSerArgTyrValArgLeu	980
Qy	2995	CGCCAGCGCCTCTGCCGCCAGAGTGTCTCTCTGGCCCCACCAGCCCCGTGGGCAGGGC	3054
Db	981	ArgGlnArgLeuCysArgGlnSerValLeuLeuTrpProHisGlnProArgGlyGlnGly	1000
Qy	3055	AGCTTCTGGGCCCAGCTGGGCACAGCCCTGACCAGGGACAACCGCCACTTCTATAACCGG	3114
Db	1001	SerPheTrpAlaGlnLeuGlyThrAlaLeuThrArgAspAsnHisHisPheTyrAsnArg	1020
Qy	3115	AACTTCTGCCGGGGCCCCACGACAGCCGAA	3144
Db	1021	AsnPheCysArgGlyProThrThrAlaGlu	1030